

[illegible]

Potential cysteine attachment sites are indicated in boldface.

SEQ ID NO:1

cph2 Locus SLL0821 (Manabe K, Nakazawa M. *J Plant Res.* 110: 109-122 (1977))

SEQ ID NO: 2

MNPNRSLEDFLRNVINKFHRALTLRETQVIVEEARIFLGVDRVKIYKFASDGSGEVL
AEAVNRAALPSLGLHFVEDIPPQAREELGNQRKMIAVDVAHRRKKSHELSGRISP
TEHSNGHYTTVDSCHIQYLLAMGVLSSLTVPVMQDQOLGIMAVHHSKPRRFTEQ
EWETMALLSKEVSLAITQSLSRQVHQQVQEALVQRLETTVAQYGDRPETWQYA
LETVGOAVEADGAVLYIAPDLTGSVAOHYQWNLRFDWGNWLETSLWQELMRGOP

SAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAE
 NFQSFLIVPLAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWREETQ
 KLVPTWNRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRLT
 LALLDALYEGKMVGVLVIAMDRFKRINESFGHKTGDGLLQEVAADRLNQKLSPLAA
 YSPLLSRWHGDGFTILLTOISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTA
 PYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTN
 QEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQW
 VLETACATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDLEL
 EITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVN
 DLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYFLTRPL
 PAEAMMTYLYPEQILDGPTPLPKVALPETETEAGQGNVGDRPLPNSLNRENPWTE
 KLHDYVLLKERLQQRNVKEKLVLKIANKIRASLNINDILYSTVTEVRQFLNTDRVVL
FKFNSQWSGQVVTESHNDFCRSIINDEIDDPCFKGHYLRLYREGRVRAVSDIEKADL
ADCHKELLRHYQVKANLVVPVVFNEENLWGLLIAHECKTPRYWQEEDLQLLMELAT
QVAIAIHQGELYEQLETANIRLQQISSLDALTQVGNRYLFDSTLEREWQRLQRIREPL
 ALLLCDVDFFKGFNDNYGHPAGDRCLKKIADAMAKVAKRPTDLVARYGGEEFAILL
 SETSLEGAINVTEALQVEVANLAIPHTVSGTGHVTLSIGIAVYTPERHINPNALVKAA
 DLALYEAKAKGRNQWLAYEGSQLPHVDGEV

Cph3. Locus SLL1473 (RcaE Homolog) a 297 aa histidine kinase homolog

SEQ ID NO: 3

MGKFLPIEFVFLAIAMTCYLWHRQNQERRRIEISIKQQTQRRERFINQITQHIRQSLNLE
TVLNTTVAEVKTLQVDRVLIYRIWQDGTGSAITESVNANYPSILGRIFSDEVFPVEY
HQAYTKGKVRAINDIDQDDIEICLADFVKQFGVKSKLVVPILQHNRASSLDNESEFP
YLWGLLITHQCATRPWQPWEVELMKQLANQVAIAIQQSELYEQLQQLNKDLENR
 VEKRTQQLAATNQSLRMEISERQKTEAALRHTNHTLQSLIAASPRGIFTNLADQIQI
 WNPTAERIFGWTETETIIAHPPELLTSNILLEDYQQFKQKVLSGMVSPSLELKCQKKDGS
 WIEIVLSAAPLLDSEENIAGLVAVVADITEQKRQAEQIRLLQSVVNTNDAAVVITEAE
 PIDDPGPRILYVNEAFTKITGYTAEEMLGKTPRVLQGPKTSRTELDRVRQAISQWQS
 VTVEAEVLNDSYKEKKSPLK

**cph4 Locus SLL1124 (DivJ homolog; PAS domain) A 1372 aa protein
that is more similar to rcaE than to cph1 [Wilde *et al.* FEBS Lett 406: 89-92 (1997).
GB:U67397 (D90905 or SLL1124)**

SEQ ID NO: 4

MTFAATPREVTASAIQWACLCLPGELSAAEALNRWHRHGQRSWEPP
AEAKAFPPWALVLDNDGQLLGLLPDWQLAAALWTEHFSPAIALAELCLPCSLRLDL
EKLPSLGEVMQIFATWGYGWDVIPVADRQHQTWGLLSIGNLIRSVNLCQLWQNLPL
QVTASPPLCLGTETTLGELVHHCFERQISSFPVVYSSPLLPAAPRIPLGNVSLSNYFK
GPNYGSGLDNPIGPDLSPTFPLCTINQTYCHARELLRRQNDDYVIITNISGA FVGWV
GPQQWLATVQPDVLEALQREVEMPRIVQHLEARIVWQQQQQQRNQHLIQKLLSR
NPNLIYLYDLVKNEIVYLNIPGSLDEGGSGGAPIPNPMVETDPRQDLLPPRYFGLEE
LAALQAHEKKEFNFEFTDGGQSVHYFVVEISAFEIDGSGQTSKILCLAQDVSHGKRA
EAALHTKEQQLQTLVNTIADGIVILDNHDKVYIANPMACQMFGLSKEEFLQSQLGLS
NRGQTEIGINVSPEEEGIGEIKAVPIHWQGEDCRLVTVRDVTDRQRVLKCLRDSQIH
RSLLEALPNLVWRLSSAGDVWECNQRTLAYFGRRGRKILGNTWQQFIEPGERENVQ
RQWRQGIAAQEFFQLECLWRSDGQYRWHLQVLPLED RFGSINGWLASSTDIDDL
KEAEKALRNQAQKEKLLSSISQRIRESLKLETILRTTVTEVRRTIHADRVLIHHIQEDG
LGT TIAESV VNGQPSVMQMDLSPESFPPECYQRYLNGYIYASRDQLPDCAINCAVQC
FTVAESQSRIVAPIVFDHSLWGLLIVHQCSSSR TWQTAEIQLMQSLGNQLAIAIQQSL
LYERLQEELSERQRAEQKLLLEVNLQKGIFDVANYMIISTDRRGIISTFNRTAEEILGY
TAAELIGQQTPLIFHDQEEMASEAVQLSQQLQQTIRPNSIDMFAIPAIQWGVYEREW
YITKTGDRLPVYVSITALRDDQGKVDGLVGVITDLRRQKQIERERQNLDFVVKNSTE
LIVITDLEQKVTFNLQAGQSLIGLENPETAQTTYLSEHISPEYLNFWQMEIIPQVFRSG
AWEGEFSLQHYQTAVEIPVTASVFLQGVNGQH PANLVAIVHDITHIKNAEKRI LAA
LEAEKELGELRSRFISTTSHEFRTPLAISSSTGILKKYWPKLDGQRRGQH LERIEESVH
HMVELLDDVLTINRAETKYLPFEPQPLDLVSFCRGITDELQSSTEYHGLLFSYDGLGP
GEIVAFDPKLLRQILTNLLGNAIKYSPSGQPVEFHLQRRGDVGIFSVQDHGIGIGPEDI
PNLFDSFYRGTNVGSIPGTGLGLPIVKKCAELHGGMITVTSQLGQGS RF EVELPLWY
S

**cph5 Locus SLL0041 (locus 1001300) An 891 aa protein, methyl-accepting
chemotaxis protein I. Homology to tsr in last 250 amino acid residues. GB:D64006 Bilin
Binding domain residues 386-550**

SEQ ID NO: 5

MAEAFIAENTAVEDVSPNPNPAIDTDALAALTQSAVELTPPPPINLPKV
ELPPMQPLAPLMAIADPDNLSPMSTSIQAPTQSGGLSLRNKAVLIALLIGLIPAGVIGG
LNLSSVDRLPVPQTEQQVKDSTTKQIRDQILIGLLVTAVGAAFVAYWMVGENTKAQ
TALALKAKHSHRNLDQPLAVAGDELAIDQTIDALSAQVEKLRHQDLSLKQAELL
TELSRANLSDIDEIQGVIQKNLDQARALFGCERLVFYYHPRYQPEAMVVQALDLTTQ
GLIDSKDHPWPWGQEDMPSQIVAINDTSGASISNPHRQWLEQHQVKASLTVPLHRDN
YPLGLLMAHHCQRPHQWEMRERQFLQQLTEELQTTLDRANLIQERNESAQQAQILK
ELTLKISAAINSEQVFDIAAQEIRLALKADRVIVYRFDATWAGTVIVESVAEGYPKAL
GATIADPCFADSYVEKYRSGRIQATRDIYNAGLTPCHIGQLKPFVKANLVAPINYK
GNLLGLLIAHQCSGPRDWHQNEIDLFGQLTVQVGLALERSDLLAQQKIAEVEQRQM
REKMQKRALELLMEVDPVSRGDLTIRAHVTEDEIGTIADSYNATIESLRRIVTQVQT
AASQFTETTDNEVAVRQLAQQANRQALDVAEALERLQAMNKSIQAVAENAAQAE
SAVQRATQTVDQGEDAMNRTVDGIVAIRETVAATAKQVKRLGESSQKISKVVNLIG
SFADQTNLLALNAAIEAAHAGEEGRGFVVADEVRSLARQSAEATAEIAQLVATIQ
AETNEVVNAMEAGTEQVVVGTKLVEETRRSLNQITAVSAQISGLVEAITSAAIEQSQ
TSESVTQTMALVAQIADKNSSEASGVSATFKELLAVAQSLQEAVKQFKVQ

**cph6 locus SLR1212 (ETR1 homolog; PAS domain) An 844 aa protein,
chromophore domain 461-628**

SEQ ID NO: 6

MAITAFTLGDFFQANSYIPHGHCYLWOTPLVWLHVSADFFTAIAYYSI
PLTLLYFLRKRQDIPFPNIIFLSTFILCCGTSHFFDIITLWYPIYWISGTVKASMAIVSII
TVFELIQIVPNALNLKSPTTELATLNLALNQEIKERQTAEIALQELNNNLEKRVEDRTT
QLAKINQQLEQEIEDKTRAKEDLEKNKDQLAQLAAIVESSQDAIISKTLDGNITSWNE
SAERLFGYTAEEMIGSHITKLIPEELILEEDLIAECIRQQQRINTYETQRQRKDGTKIDV
ALTISPIRDEHKNVVGASKIVRDITARLDVENALRESQYPIEKLANYSPQILYILDPIA
WKNIYVNYQSFEILGYTPEEFKNGGTELLLNIVHPDDIPTLYENKNFWQKSQEGQVL

**Cph8 locus SLR1969, a 750 aa protein. CHROMOPHORE DOMAIN
(156-347). Contains a histidine kinase transmitter domain. Adenylate cyclase homology**

SEQ ID NO: 8

MLPAFSPIFRLLPAVTFRLLRFWRTLAQQTGDGVQCFVGDLPSSLK
PPGPSVLEAEVDHRFALLVSPGQWALLEGEQISPHHYAVSITFAQGIIEDFIQKQNL
VVAEAMPHRPETPSGPTIAEQLTLGLLEILNSDSTSFSPEPSLQDSLQASQVKLLSQVI
AQIRQSLDLSEILNNAVTAVQKFLFVDRLVIYQFHYSQPSLTPLEENQIPAPRPRQQY
GEVTYEARRSPEIDTMLGIMTENDCFSQVFSYEQKYLKGAVVAVSDIENHYSSSYCL
VGLLQRYQVRAKLVAPIIVEGQLWGLLIAHQCHHPRQWLDSEKNFLGQIGEHLAVA
IVQSLLYSEVQKQKNNFEKRVIERTKELRDTLMAAQAANLLKSQFINNISHELRTPLT
SIIGLSATLLRWFDHPASLPPAKQQYYLLNIQENGKKLLDQINSIIQLSQLESGQTALN
CQSFSLHTLAQTVIHSLLGVAIKQQINLELDYQINVGQDQFCADQERLDQILTQLLNN
ALKFTPAGTVILRIWKESNQAIFQVEDTGIGINEQQLPVLFEAFKVAGDSYTSFYET
GGVGLALTKQLVELHGGYIEVESSPGQGTFITTVIQQNFPPTTKGQVQDKLDAAMP
FNSSVIVIEQDEEIATLICELLTVANYQVIWLIDTTNALQQVELLQPGLIIVDGDGFVDV
TEVTRGIKKSRISKVTVFLLSESLSSAEWQALSQKGIDDYLLKPLQPELLLQRVQSIQ
QEPLR

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